

*re-run*

IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/700,249

DATE: 09/10/2004

TIME: 14:19:34

Input Set : N:\AMC\US10700249.raw

Output Set: N:\CRF4\09102004\J700249.raw

1 <110> APPLICANT: Matsui, Toshimitsu  
 2 Aaronson, Stuart A.  
 3 Pierce, Jacalyn H.  
 4 <120> TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor

5 <130> FILE REFERENCE: 14014.0266U2  
 6 <140> CURRENT APPLICATION NUMBER: US/10/700,249  
 7 <141> CURRENT FILING DATE: 2003-10-31  
 8 <150> PRIOR APPLICATION NUMBER: US/09/769,987  
 9 <151> PRIOR FILING DATE: 2001-01-25  
 10 <150> PRIOR APPLICATION NUMBER: US 08/460,656  
 11 <151> PRIOR FILING DATE: 1995-06-02  
 12 <150> PRIOR APPLICATION NUMBER: US 08/439,095  
 13 <151> PRIOR FILING DATE: 1995-05-11  
 14 <150> PRIOR APPLICATION NUMBER: US 07/915,884  
 15 <151> PRIOR FILING DATE: 1992-07-20  
 16 <150> PRIOR APPLICATION NUMBER: US 07/308,282  
 17 <151> PRIOR FILING DATE: 1989-02-09  
 18 <160> NUMBER OF SEQ ID NOS: 2  
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0



21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 6412  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =  
 27 synthetic construct  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (139)...(3406)  
 31 <400> SEQUENCE: 1

32	ccattactgt tggagctaca gggagagaaa caggaggaga ctgcaagaga tcatttgga	60
33	aggccgtggg cacgctcttt actccatgtg tgggacattc attgcggaat aacatcgga	120
34	gagaagtttc ccagagct atg ggg act tcc cat ccg gcg ttc ctg gtc tta	171
35	Met Gly Thr Ser His Pro Ala Phe Leu Val Leu	
36	1 5 10	
37	ggc tgt ctt ctc aca ggg ctg agc cta atc ctc tgc cag ctt tca tta	219
38	Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu	
39	15 20 25	
40	ccc tct atc ctt cca aat gaa aat gaa aag gtt gtg cag ctg aat tca	267
41	Pro Ser Ile Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser	
42	30 35 40	
43	tcc ttt tct ctg aga tgc ttt ggg gag agt gaa gtg agc tgg cag tac	315
44	Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr	

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45	45	50	55	
46	ccc atg tct gaa gaa gag agc tcc gat gtg gaa atc aga aat gaa gaa	363		
47	Pro Met Ser Glu Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu			
48	60	65	70	75
49	aac aac agc ggc ctt ttt gtg acg gtc ttg gaa gtg agc agt gcc tcg	411		
50	Asn Asn Ser Gly Leu Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser			
51	80	85	90	
52	gcg gcc cac aca ggg ttg tac act tgc tat tac aac cac act cag aca	459		
53	Ala Ala His Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr			
54	95	100	105	
55	gaa gag aat gag ctt gaa ggc agg cac att tac atc tat gtg cca gac	507		
56	Glu Glu Asn Glu Leu Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp			
57	110	115	120	
58	cca gat gta gcc ttt gta cct cta gga atg acg gat tat tta gtc atc	555		
59	Pro Asp Val Ala Phe Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile			
60	125	130	135	
61	gtg gag gat gat gat tct gcc att ata cct tgt cgc aca act gat ccc	603		
62	Val Glu Asp Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro			
63	140	145	150	155
64	gag act cct gta acc tta cac aac agt gag ggg gtg gta cct gcc tcc	651		
65	Glu Thr Pro Val Thr Leu His Asn Ser Glu Gly Val Val Pro Ala Ser			
66	160	165	170	
67	tac gac agc aga cag ggc ttt aat ggg acc ttc act gta ggg ccc tat	699		
68	Tyr Asp Ser Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr			
69	175	180	185	
70	atc tgt gag gcc acc gtc aaa gga aag aag ttc cag acc atc cca ttt	747		
71	Ile Cys Glu Ala Thr Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe			
72	190	195	200	
73	aat gtt tat gct tta aaa gca aca tca gag ctg gat cta gaa atg gaa	795		
74	Asn Val Tyr Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu			
75	205	210	215	
76	gct ctt aaa acc gtg tat aag tca ggg gaa acg att gtg gtc acc tgt	843		
77	Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys			
78	220	225	230	235
79	gct gtt ttt aac aat gag gtg gtt gac ctt caa tgg act tac cct gga	891		
80	Ala Val Phe Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly			
81	240	245	250	
82	gaa gtg aaa ggc aaa ggc atc aca atg ctg gaa gaa atc aaa gtc cca	939		
83	Glu Val Lys Gly Lys Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro			
84	255	260	265	
85	tcc atc aaa ttg gtg tac act ttg acg gtc ccc gag gcc acg gtg aaa	987		
86	Ser Ile Lys Leu Val Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys			
87	270	275	280	
88	gac agt gga gat tac gaa tgt gct gcc cgc cag gct acc agg gag gtc	1035		
89	Asp Ser Gly Asp Tyr Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val			
90	285	290	295	
91	aaa gaa atg aag aaa gtc act att tct gtc cat gag aaa ggt ttc att	1083		
92	Lys Glu Met Lys Lys Val Thr Ile Ser Val His Glu Lys Gly Phe Ile			
93	300	305	310	315

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94	gaa atc aaa ccc acc ttc agc cag ttg gaa gct gtc aac ctg cat gaa	1131
95	Glu Ile Lys Pro Thr Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu	
96	320 325 330	
97	gtc aaa cat ttt gtt gta gag gtg cgg gcc tac cca cct ccc agg ata	1179
98	Val Lys His Phe Val Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile	
99	335 340 345	
100	tcc tgg ctg aaa aac aat ctg act ctg att gaa aat ctc act gag atc	1227
101	Ser Trp Leu Lys Asn Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile	
102	350 355 360	
103	acc act gat gtg gaa aag att cag gaa ata agg tat cga agc aaa tta	1275
104	Thr Thr Asp Val Glu Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu	
105	365 370 375	
106	aag ctg atc cgt gct aag gaa gaa gac agt ggc cat tat act att gta	1323
107	Lys Leu Ile Arg Ala Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val	
108	380 385 390 395	
109	gct caa aat gaa gat gct gtg aag agc tat act ttt gaa ctg tta act	1371
110	Ala Gln Asn Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr	
111	400 405 410	
112	caa gtt cct tca tcc att ctg gac ttg gtc gat gat cac cat ggc tca	1419
113	Gln Val Pro Ser Ser Ile Leu Asp Leu Val Asp Asp His His Gly Ser	
114	415 420 425	
115	act ggg gga cag acg gtg agg tgc aca gct gaa ggc acg ccg ctt cct	1467
116	Thr Gly Gly Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro	
117	430 435 440	
118	gat att gag tgg atg ata tgc aaa gat att aag aaa tgt aat aat gaa	1515
119	Asp Ile Glu Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu	
120	445 450 455	
121	act tcc tgg act att ttg gcc aac aat gtc tca aac atc atc acg gag	1563
122	Thr Ser Trp Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu	
123	460 465 470 475	
124	atc cac tcc cga gac agg agt acc gtg gag ggc cgt gtg act ttc gcc	1611
125	Ile His Ser Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala	
126	480 485 490	
127	aaa gtg gag gag acc atc gcc gtg cga tgc ctg gct aag aat ctc ctt	1659
128	Lys Val Glu Glu Thr Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu	
129	495 500 505	
130	gga gct gag aac cga gag ctg aag ctg gtg gct ccc acc ctg cgt tct	1707
131	Gly Ala Glu Asn Arg Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser	
132	510 515 520	
133	gaa ctc acg gtg gct gct gca gtc ctg gtg ctg ttg gtg att gtg atc	1755
134	Glu Leu Thr Val Ala Ala Val Leu Val Leu Leu Val Ile Val Ile	
135	525 530 535	
136	atc tca ctt att gtc ctg gtt gtc att tgg aaa cag aaa ccg agg tat	1803
137	Ile Ser Leu Ile Val Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr	
138	540 545 550 555	
139	gaa att cgc tgg agg gtc att gaa tca atc agc ccg gat gga cat gaa	1851
140	Glu Ile Arg Trp Arg Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu	
141	560 565 570	
142	tat att tat gtg gac ccg atg cag ctg cct tat gac tca aga tgg gag	1899

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143	Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu	
144	575 580 585	
145	ttt cca aga gat gga cta gtg ctt ggt cgg gtc ttg ggg tct gga gcg	1947
146	Phe Pro Arg Asp Gly Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala	
147	590 595 600	
148	ttt ggg aag gtg gtt gaa gga aca gcc tat gga tta agc cgg tcc caa	1995
149	Phe Gly Lys Val Val Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln	
150	605 610 615	
151	cct gtc atg aaa gtt gca gtg aag atg cta aaa ccc acg gcc aga tcc	2043
152	Pro Val Met Lys Val Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser	
153	620 625 630 635	
154	agt gaa aaa caa gct ctc atg tct gaa ctg aag ata atg act cac ctg	2091
155	Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Thr His Leu	
156	640 645 650	
157	ggg cca cat ttg aac att gta aac ttg ctg gga gcc tgc acc aag tca	2139
158	Gly Pro His Leu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser	
159	655 660 665	
160	ggc ccc att tac atc atc aca gag tat tgc ttc tat gga gat ttg gtc	2187
161	Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val	
162	670 675 680	
163	aac tat ttg cat aag aat agg gat agc ttc ctg agc cac cac cca gag	2235
164	Asn Tyr Leu His Lys Asn Arg Asp Ser Phe Leu Ser His His Pro Glu	
165	685 690 695	
166	aag cca aag aaa gag ctg gat atc ttt gga ttg aac cct gct gat gaa	2283
167	Lys Pro Lys Lys Glu Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu	
168	700 705 710 715	
169	agc aca cgg agc tat gtt att tta tct ttt gaa aac aat ggt gac tac	2331
170	Ser Thr Arg Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr	
171	720 725 730	
172	atg gac atg aag cag gct gat act aca cag tat gtc ccc atg cta gaa	2379
173	Met Asp Met Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu	
174	735 740 745	
175	agg aaa gag gtt tct aaa tat tcc gac atc cag aga tca ctc tat gat	2427
176	Arg Lys Glu Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp	
177	750 755 760	
178	cgt cca gcc tca tat aag aag aaa tct atg tta gac tca gaa gtc aaa	2475
179	Arg Pro Ala Ser Tyr Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys	
180	765 770 775	
181	aac ctc ctt tca gat gat aac tca gaa ggc ctt act tta ttg gat ttg	2523
182	Asn Leu Leu Ser Asp Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu	
183	780 785 790 795	
184	ttg agc ttc acc tat caa gtt gcc cga gga atg gag ttt ttg gct tca	2571
185	Leu Ser Phe Thr Tyr Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser	
186	800 805 810	
187	aaa aat tgt gtc cac cgt gat ctg gct gct cgc aac gtc ctc ctg gca	2619
188	Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala	
189	815 820 825	
190	caa gga aaa att gtg aag atc tgt gac ttt ggc ctg gcc aga gac atc	2667
191	Gln Gly Lys Ile Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile	

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192					830													840		
193	atg	cat	gat	tgc	aac	tat	gtg	tgc	aaa	ggc	agt	acc	ttt	ctg	ccc	gtg			2715	
194	Met	His	Asp	Ser	Asn	Tyr	Val	Ser	Lys	Gly	Ser	Thr	Phe	Leu	Pro	Val				
195		845					850					855								
196	aag	tgg	atg	gct	cct	gag	agc	atc	ttt	gac	aac	ctc	tac	acc	aca	ctg			2763	
197	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asp	Asn	Leu	Tyr	Thr	Thr	Leu				
198	860					865				870					875					
199	agt	gat	gtc	tgg	tct	tat	ggc	att	ctg	ctc	tgg	gag	atc	ttt	tcc	ctt			2811	
200	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu				
201					880					885					890					
202	ggg	ggc	acc	cct	tac	ccc	ggc	atg	atg	gtg	gat	tct	act	ttc	tac	aat			2859	
203	Gly	Gly	Thr	Pro	Tyr	Pro	Gly	Met	Met	Val	Asp	Ser	Thr	Phe	Tyr	Asn				
204				895				900						905						
205	aag	atc	aag	agt	ggg	tac	cgg	atg	gcc	aag	cct	gac	cac	gct	acc	agt			2907	
206	Lys	Ile	Lys	Ser	Gly	Tyr	Arg	Met	Ala	Lys	Pro	Asp	His	Ala	Thr	Ser				
207		910					915					920								
208	gaa	gtc	tac	gag	atc	atg	gtg	aaa	tgc	tgg	aac	agt	gag	ccg	gag	aag			2955	
209	Glu	Val	Tyr	Glu	Ile	Met	Val	Lys	Cys	Trp	Asn	Ser	Glu	Pro	Glu	Lys				
210		925				930					935									
211	aga	ccc	tcc	ttt	tac	cac	ctg	agt	gag	att	gtg	gag	aat	ctg	ctg	cct			3003	
212	Arg	Pro	Ser	Phe	Tyr	His	Leu	Ser	Glu	Ile	Val	Glu	Asn	Leu	Leu	Pro				
213	940				945				950					955						
214	gga	caa	tat	aaa	aag	agt	tat	gaa	aaa	att	cac	ctg	gac	ttc	ctg	aag			3051	
215	Gly	Gln	Tyr	Lys	Lys	Ser	Tyr	Glu	Lys	Ile	His	Leu	Asp	Phe	Leu	Lys				
216				960				965						970						
217	agt	gac	cat	cct	gct	gtg	gca	cgc	atg	cgt	gtg	gac	tca	gac	aat	gca			3099	
218	Ser	Asp	His	Pro	Ala	Val	Ala	Arg	Met	Arg	Val	Asp	Ser	Asp	Asn	Ala				
219				975				980						985						
220	tac	att	ggg	gtc	acc	tac	aaa	aac	gag	gaa	gac	aag	ctg	aag	gac	tgg			3147	
221	Tyr	Ile	Gly	Val	Thr	Tyr	Lys	Asn	Glu	Glu	Asp	Lys	Leu	Lys	Asp	Trp				
222		990					995					1000								
223	gag	ggg	ggg	ctg	gat	gag	cag	aga	ctg	agc	gct	gac	agt	ggc	tac	atc			3195	
224	Glu	Gly	Gly	Leu	Asp	Glu	Gln	Arg	Leu	Ser	Ala	Asp	Ser	Gly	Tyr	Ile				</

RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

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